PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/973,815*

DATE: 06/21/1999
TIME: 14:24:53

INPUT SET: S32263.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
                                    SEQUENCE LISTING           ENTERED
 1
 2
 3    (1)    General Information:
 4
 5         (i) APPLICANT:
 6             (A) NAME: Deutsches Krebsforschungszentrum Stiftung des
 7                       ffentlichen Rechts
 8             (B) STREET: Im Neuenheimer Feld 280
 9             (C) CITY: Heidelberg
10             (E) COUNTRY: Germany
11             (F) POSTAL CODE: 69120
12
13         (ii) TITLE OF INVENTION: DNase active Protein
14
15        (iii) NUMBER OF SEQUENCES: 3
16
17         (v) COMPUTER-READABLE FORM:
18             (A) MEDIUM TYPE: Floppy disk
19             (B) COMPUTER: IBM PC compatible
20             (C) OPERATING SYSTEM: PC-DOS/MS-DOS
21             (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)
22
23        (vi) CURRENT APPLICATION DATA:
24             (A) APPLICATION NUMBER:
25             (B) FILING DATE:
26
27       (vii) PRIOR APPLICATION DATA:
28             (A) APPLICATION NUMBER:  PCT/DE96/01016
29             (B) FILING DATE:
30
31             (A) APPLICATION NUMBER: DE 195 21 046.8
32             (B) FILING DATE: 09-JUN-1995
33
34
35    (2) INFORMATION FOR SEQ ID NO: 1:
36
37         (i) SEQUENCE CHARACTERISTICS:
38             (A) LENGTH: 2661 Base pairs
39             (B) TYPE: Nucleotide
40             (C) STRANDEDNESS: double
41             (D) TOPOLOGY: linear
42
43        (ii) MOLECULE TYPE: cDNA
44
45
46        (ix) FEATURE:
```

INPUT SET: S32263.raw

```
47              (A) NAME/KEY: CDS
48              (B) LOCATION:795..1700
49
50
51      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
52
53  CTTGAACGCC TGACCTCGTA TCCACCCGCC TCAGCCTCCC AAAGTGCTGG GATTACAGGC         60
54
55  ATGAGCCACC ACGCCCAGCC CATAATTTAT TGATTTTTTA AAATTTGTCC AGCCTTCTAT        120
56
57  TACCACGTCG AATCCATTAG CTACAGCCAT CCCATGAGAA GCTGAGTGGA TTCAGCCCCA        180
58
59  CCTCCTGCTC ACAGACCCTG TCCGAGCACC TCATTTGTCC CAACAGCATT ACTGCAGGAC        240
60
61  CCCCAGGACG TTGGACTGCC AGCTCCCTGG GTCTCCTCCT CTCTGGGGCA GATCCTCAGT        300
62
63  CCTCCCTTGA CTTCACGACT GTGGCCAGAT CATGTGTGGA CTGTCCCTCT CTTTGGGTCT        360
64
65  CCAGAGCGCT TGCATCAAAC ACCCCTAACT CAGAAGTGTG CAGCCACACT GGGACTCAGA        420
66
67  ACCCAACAAC AGGGACAGAA GACTCACGCC CTTGGGGTGC CCGGTCTCGT GGCATCAGGC        480
68
69  ATGACTTCCA GCTCCTGCGC CTTCCCCAGC AACTGCTGAC TGGGGACCCA GACCGGGAGC        540
70
71  TGAGCGACGG GCCTGGCGAG CGAAGCTCGG GGTCTCACTC AGGCACCAGC CCCTCCTTGC        600
72
73  CCCAGGCTTG AGTGACTCAC AGCCCTATTC AGGCAGGAGC TGCTCTTCTG GGGTATCGCG        660
74
75  ATCCACTTAA GGATGAGGCA GACTTGGTGA CAAGCTGGTC TGAGCAGCGC TTCCAGAGCC        720
76
77  AGAACTGAGC CCAGTGAGAG CGCACCCTGG AGCAGCCTGG ATTCCTGGGG TGTCCCCGGC        780
78
79  AGCCACACAC AGCC ATG CAC TAC CCA ACT GCA CTC CTC TTC CTC ATC CTG        830
80                   Met His Tyr Pro Thr Ala Leu Leu Phe Leu Ile Leu
81                    1               5                   10
82
83  GCC AAT GGG GCC CAG GCC TTT CGC ATC TGC GCC TTC AAT GCC CAG CGG        878
84  Ala Asn Gly Ala Gln Ala Phe Arg Ile Cys Ala Phe Asn Ala Gln Arg
85           15                  20                  25
86
87  CTG ACA CTG GCC AAG GTG GCC AGG GAG CAG GTG ATG GAC ACC TTA GTT        926
88  Leu Thr Leu Ala Lys Val Ala Arg Glu Gln Val Met Asp Thr Leu Val
89       30                  35                  40
90
91  CGG ATA CTG GCT CGC TGT GAC ATC ATG GTG CTG CAG GAG GTG GTA GAC        974
92  Arg Ile Leu Ala Arg Cys Asp Ile Met Val Leu Gln Glu Val Val Asp
93   45                  50                  55                  60
94
95  TCT TCC GGC AGC GCC ATC CCC CTC CTG CTT CGA GAA CTC AAT CGA TTT       1022
96  Ser Ser Gly Ser Ala Ile Pro Leu Leu Leu Arg Glu Leu Asn Arg Phe
97                   65                  70                  75
98
99  GAT GGC TCT GGG CCC TAC AGC ACC CTG AGC AGC CCC CAG CTG GGG CGC       1070
```

```
100    Asp Gly Ser Gly Pro Tyr Ser Thr Leu Ser Ser Pro Gln Leu Gly Arg
101             80                  85                  90
102

103    AGC ACC TAC ATG GAG ACG TAT GTG TAC TTC TAT CGG TCA CAC AAA ACA      1118
104    Ser Thr Tyr Met Glu Thr Tyr Val Tyr Phe Tyr Arg Ser His Lys Thr
105         95                  100                 105
106

107    CAG GTC CTG AGT TCC TAC GTG TAC AAC GAT GAG GAT GAC GTC TTT GCC      1166
108    Gln Val Leu Ser Ser Tyr Val Tyr Asn Asp Glu Asp Asp Val Phe Ala
109         110                 115                 120
110

111    CGG GAG CCA TTT GTG GCC CAG TTC TCT TTG CCC AGC AAT GTC CTT CCC      1214
112    Arg Glu Pro Phe Val Ala Gln Phe Ser Leu Pro Ser Asn Val Leu Pro
113    125                 130                 135                 140
114

115    AGC CTG GTG TTG GTC CCG CTG CAC ACC ACT CCT AAG GCC GTA GAG AAG      1262
116    Ser Leu Val Leu Val Pro Leu His Thr Thr Pro Lys Ala Val Glu Lys
117             145                 150                 155
118

119    GAG CTG AAC GCC CTC TAC GAT GTG TTT CTG GAG GTC TCC CAG CAC TGG      1310
120    Glu Leu Asn Ala Leu Tyr Asp Val Phe Leu Glu Val Ser Gln His Trp
121             160                 165                 170
122

123    CAG AGC AAG GAC GTG ATC CTG CTT GGG GAC TTC AAT GCT GAC TGC GCT      1358
124    Gln Ser Lys Asp Val Ile Leu Leu Gly Asp Phe Asn Ala Asp Cys Ala
125             175                 180                 185
126

127    TCA CTG ACC AAA AAG CGC CTG GAC AAG CTG GAG CTG CGG ACT GAG CCA      1406
128    Ser Leu Thr Lys Lys Arg Leu Asp Lys Leu Glu Leu Arg Thr Glu Pro
129         190                 195                 200
130

131    GGC TTC CAC TGG GTG ATT GCC GAT GGG GAG GAC ACC ACA GTG CGG GCC      1454
132    Gly Phe His Trp Val Ile Ala Asp Gly Glu Asp Thr Thr Val Arg Ala
133    205                 210                 215                 220
134

135    AGC ACC CAC TGC ACC TAT GAC CGC GTC GTG CTG CAC GGG GAG CGC TGC      1502
136    Ser Thr His Cys Thr Tyr Asp Arg Val Val Leu His Gly Glu Arg Cys
137             225                 230                 235
138

139    CGG AGT CTG CTG CAC ACT GCG GCT GCC TTT GAC TTC CCC ACG AGC TTC      1550
140    Arg Ser Leu Leu His Thr Ala Ala Ala Phe Asp Phe Pro Thr Ser Phe
141             240                 245                 250
142

143    CAG CTC ACC GAG GAG GAG GCC CTC AAC ATC AGT GAC CAC TAC CCC GTG      1598
144    Gln Leu Thr Glu Glu Glu Ala Leu Asn Ile Ser Asp His Tyr Pro Val
145         255                 260                 265
146

147    GAG GTG GAG CTG AAG CTG AGC CAG GCG CAC AGC GTC CAG CCT CTC AGC      1646
148    Glu Val Glu Leu Lys Leu Ser Gln Ala His Ser Val Gln Pro Leu Ser
149         270                 275                 280
150

151    CTC ACT GTT CTG TTG CTG CTA TCA CTC CTG TCC CCT CAG CTG TGC CCT      1694
152    Leu Thr Val Leu Leu Leu Leu Ser Leu Leu Ser Pro Gln Leu Cys Pro
```

INPUT SET: S32263.raw

```
153    285              290              295              300
154
155    GCT GCC TGAGCGTCCC CCTACCCCCC CAGGGCCTGC TGCCTTTTGG GACTTAAACC       1750
156    Ala Ala
157
158
159    CCAGCCTCCC CCGTCCATCC AGCCCTGGGG CTGGGGGGCT TCAACTATAG TTGCCCTGTG       1810
160
161    ACTGTAGTCC ACCCCTGCCT GCCTTGTTTG ATTTGGCTCT TGTTCTTTGG TTGGGCTTGT       1870
162
163    GCCTAGATTA GGAGAGGAAG CCAGGGGCCC TGCACTCATG CCACCTGCCA GGTAGTGTAG       1930
164
165    TATCAGGAGT GGAGACAAAG TGGGCTCTGG GTTGGGGTAG GGGAAGGGAG GGTTCAGAAA       1990
166
167    GAGGAATGAA GATGTTGTAT GACAAGAAGG AAAGTTACTG AGAACAAAAA CCCAGATTGG       2050
168
169    TGAGATAGGA CACTTGTGCA GCAGATATGC CAATGGGCCA TGTTTATTGT GGATGGGTAA       2110
170
171    GAATCACCAG GAAACCATTA AGCCCCAATA GCTACAAGGA GGGTGGTTAA TCTGCTATAT       2170
172
173    CAAACTCCTT CCCTGAAACC AGCAAACACC GGGAAACATT TTGGCTCATT ATAATCCGGT       2230
174
175    GAACAATGCA GTCAGGCCTG TTATAACCGC TGAGCAGCCA CACTCGCACC TCCTGGGTGC       2290
176
177    TGTAGTCTGT GTTGGTACAG GCTTCTGCAT GCCTGGTAAA GTCCAGCCAA GGCTGGTCAA       2350
178
179    GGCAACATCT CCACACAGAA AATCTGCACC AGTTATGTAA GCTAAAAAGC TGTGTGAACC       2410
180
181    CAGGTGTCCC GGAAAGGGGC TGCAGGACAC AGCAAAATGC CAGCAGCGTG CCGGACCCCT       2470
182
183    CCCTTCCATC CTCCTCTCCA AGAACAGAG GTCAGGAAAA ACACTGGCTG GGACGCTAGA       2530
184
185    AGGGTCATGT GTTAACTATA ATCACATTTA TGGTTTGGAA CCATCACCCC AAGGTAAAAA       2590
186
187    AAAAAATAAA AGGTATGTTT GGCAAAATAA AATAAAGGTA ATTAAAAACC TAAAAAAAAA       2650
188
189    AAAAAAAAAA A                                                           2661
190
191
192    (2) INFORMATION FOR SEQ ID NO: 2:
193
194        (i) SEQUENCE CHARACTERISTICS:
195            (A) LENGTH: 43 Base pairs
196            (B) TYPE: Nucleotide
197            (C) STRANDEDNESS: single
198            (D) TOPOLOGY: linear
199
200        (ii) MOLECULE TYPE: other nucleic acid
201            (A) DESCRIPTION:  /desc = "DNA-Primer"
202
203        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
204
205    CAGGGATCCG ATGACGATGA CAAAATGCAC TACCCAACTG CAC                          43
```

INPUT SET: S32263.raw

```
206
207
208    (2) INFORMATION FOR SEQ ID NO: 3:
209
210        (i) SEQUENCE CHARACTERISTICS:
211            (A) LENGTH: 27 Base pairs
212            (B) TYPE: Nucleotide
213            (C) STRANDEDNESS: single    .
214            (D) TOPOLOGY: linear
215
216        (ii) MOLECULE TYPE: other nucleic acid
217            (A) DESCRIPTION:  /desc = "DNA-Primer"
218
219        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
220
221    GGGGGATCCT CAGGCAGCAG GGCACAG                                  27
222
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/973,815*

INPUT SET: S32263.raw

Line	Error	Original Text
5	Mandatory Value Not Present	(i) APPLICANT:
6	Unknown or Misplaced Identifier	(A) NAME: Deutsches Krebsforschungszentrum Stiftung de
8	Unknown or Misplaced Identifier	(B) STREET: Im Neuenheimer Feld 280
9	Unknown or Misplaced Identifier	(C) CITY: Heidelberg
10	Unknown or Misplaced Identifier	(E) COUNTRY: Germany
11	Unknown or Misplaced Identifier	(F) POSTAL CODE: 69120